

F:151-163/Product: neurotensin #status experimental <NTS>
F:151/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime

Query Match 89.2%; Score 794; DB 1; Length 170;
Best Local Similarity 90.0%; Pred. No. 9.6e-65;
Matches 153; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MMAGMKIQLVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
Db 1 MMAGMKIQLVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKASVSSWKMTLLN 60
Qy 61 VCSLVNNLNSPAETGEVHEELVARRKLPALDGFSLKAMLTIIYQLHKICHSAFOHWE 120
Db 61 VCSFVNLLNSQAEETGEFREBELITRRKFPTALDGFSLKAMLTIIYQLKICHSAFOQWE 120
Qy 121 LIQEDILDTGNDKNGKEEVIRKPIYILKQRYENKPRPYILKRDSYYY 170
Db 121 LIQEDVLDAGNDKNEKEEVIRKPIYILKQRYENKPRPYILKRGSYYY 170

RESULT 2

A28146
neurotensin / neurotensin N precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 13-Mar-1997
C:Accession: A28146; A56789
R:Kislauskis, E.; Bullock, B.; McNeil, S.; Dobner, P.R.
J. Biol. Chem. 263, 4963-4968, 1988
A:Title: The rat gene encoding neurotensin and neurotensin N. Structure, tissue-specific
A:Reference number: A28146; MUID:88169625; PMID:2832414
A:Accession: A28146
A:Molecule type: mRNA
A:Residues: 1-169 <KIS>
R:Bidard, J.N.; de Nadaï, F.; Rovere, C.; Moïnier, D.; Laur, J.; Martinez, J.; Cuber, J.
Biochem. J. 291, 225-233, 1993
A:Title: Immunological and biochemical characterization of processing products from the
A:Reference number: A56789; MUID:93228610; PMID:8471039
A:Accession: A56789
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-42 <RID>
A:Experimental source: medullary thyroid carcinoma 6-23 cell extracts
A:Note: sequence extracted from NCBI backbone (NCBIP:129397)
C:Superfamily: neurotensin
C:Keywords: neuropeptide

Query Match 79.9%; Score 711; DB 2; Length 169;
Best Local Similarity 78.1%; Pred. No. 3.2e-57;
Matches 132; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

Qy 2 MAGMKIQLVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLNV 61
Db 1 MIGNMLQLVCLTLAFSSWSLCSSEEDVRLEADLLTNMHASKVSKGSPSPSWKMTLLNV 60
Qy 62 CSLVNNLNSPAETGEVHEELVARRKLPALDGFSLKAMLTIIYQLHKICHSAFOHWEL 121
Db 61 CSLINNLSAAEAGEMDLDAKRLPLVLDLDFSLKALTIVFQLKICHSAFOHWEI 120
Qy 122 IQEDILDTGNDKNGKEEVIRKPIYILKQRYENKPRPYILKRDSYYY 170
Db 121 IQEDILDTGNDKNGKEEVIRKPIYILKQRYENKPRPYILKRASYYY 169

RESULT 3

I58190
neurotensin/neurotensin N - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I58190
R:Bean, A.J.; Bagerlind, A.; Hokfelt, T.; Dobner, P.R.
Neuroscience 50, 259-268, 1992
A:Title: Cloning of human neurotensin/neurotensin N genomic sequences and expression in t
A:Reference number: I58190; MUID:93063858; PMID:1436492

A:Accession: I58190

A:Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: DNA

A:Residues: 1-120 <RES>

A:Cross-references: GB:547339; NID:g258822; PIDN:AAB23934.1; PID:g258823

C:Superfamily: neurotensin

Query Match 70.3%; Score 626; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMAGMKIQLVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
Db 1 MMAGMKIQLVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
Qy 61 VCSLVNNLNSPAETGEVHEELVARRKLPALDGFSLKAMLTIIYQLHKICHSAFOHWE 120
Db 61 VCSLVNNLNSPAETGEVHEELVARRKLPALDGFSLKAMLTIIYQLHKICHSAFOHWE 120

RESULT 4

H84830
hypothetical protein At2g40550 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84830
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84830
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <STO>
A:Cross-references: GB:AE002093; NID:g2651302; PIDN:AAB87582.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g40550
A:Map position: 2

Query Match 10.1%; Score 90; DB 2; Length 550;
Best Local Similarity 22.2%; Pred. No. 2.5;
Matches 24; Conservative 28; Mismatches 44; Indels 12; Gaps 3;

Qy 26 SEEMKALEADFLTNMHTSKISKAHV-----PSWKMTLLNVCSLVNNLNSPAETGEVH 79
Db 436 SEGKSNIMPADLVLPQPSQVNSLEVITPETAETWRCYLATCKSLSHSI---GQELQQV 492
Qy 80 EEEVLVARRKLPALDGFSLKAMLTIIYQLHKICHSR---AFQHWELIOE 124
Db 493 ENDLVAARQDTRSLGSDQLSRLLTMARMSVSYGETTSLSEHWQNVLE 540

RESULT 5

H70183
conserved hypothetical protein BB0673 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: H70183
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70183
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-171 <KLE>
A:Cross-references: GB:AE001168; NID:g2688598; PIDN:AAC67020.1; PID:g2688603
A:Experimental source: strain B31

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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:15:54 ; Search time 21 Seconds
(without alignments)
778.508 Million cell updates/sec

Title: US-09-927-565A-1

Perfect score: 890

Sequence: 1 MMAGMKIQLVCMILLAFSSW.....QLYENKRRPYILKRDVYY 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	794	89.2	170	1	neurotensin precu
2	711	79.9	169	2	neurotensin / neur
3	626	70.3	120	2	neurotensin/neurom
4	90	10.1	550	2	hypothetical prote
5	87.5	9.8	171	2	conserved hypothet
6	86.5	9.7	499	2	conserved hypothet
7	86.5	9.7	605	2	hypothetical prote
8	86.5	9.7	610	2	hypothetical prote
9	84.5	9.5	1269	2	protein W09G10.4 (
10	81.5	9.2	230	1	H+-transporting tw
11	79.5	8.9	479	2	CIL protein - vari
12	79.5	8.9	479	2	hypothetical prote
13	79.5	8.9	479	2	hypothetical prote
14	79.5	8.9	479	2	EIL protein - vari
15	79.5	8.9	651	2	hypothetical prote
16	79	8.9	811	1	hypothetical prote
17	79	8.9	819	1	endopeptidase La (
18	79	8.9	819	2	Lon ATP-dependent
19	79	8.9	1626	2	DNA topoisomerase
20	78.5	8.8	479	2	EIL protein - vacc
21	78	8.8	283	2	probable lipoprote
22	78	8.8	537	2	acrosomal protein
23	78	8.8	837	2	hypothetical prote
24	78	8.8	908	2	disease resistance
25	77	8.7	1252	2	probable type II D
26	76.5	8.6	273	2	hypothetical prote
27	76.5	8.6	377	2	hypothetical prote
28	76.5	8.6	633	2	probable mureinpep
29	76	8.5	1857	2	hypothetical prote

30	75.5	8.5	268	2	T06802
31	75.5	8.5	401	1	A36961
32	75.5	8.5	1298	2	T24480
33	75.5	8.5	2485	1	H71621
34	75	8.4	233	2	B47537
35	75	8.4	255	2	T05958
36	75	8.4	647	2	F90595
37	75	8.4	1612	2	S59969
38	74	8.3	531	2	T16263
39	74	8.3	585	2	G64220
40	73.5	8.3	371	2	C70237
41	73.5	8.3	907	2	T01764
42	73	8.2	843	2	A49922
43	73	8.2	3433	1	S28381
44	72.5	8.1	457	2	A54694
45	72	8.1	227	2	JE0203

ALIGNMENTS

RESULT 1

UNDG

neurotensin precursor - dog

N:Contains: neuromedin N; neuromedin N-125; neurotensin

C:Species: Canis lupus familiaris (dog)

C>Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 18-Jun-1999

C:Accession: A28025; B60319; A60324; JN0293; A36272

R:Dobner, P.R.; Barber, D.L.; Villa-Komaroff, L.; McKiernan, C.

Proc. Natl. Acad. Sci. U.S.A. 84, 3516-3520, 1987

A:Title: Cloning and sequence analysis of cDNA for the canine neurotensin/neuromedin N p

A:Reference number: A28025; MUID:87204168; PMID:3472221

A:Accession: A28025

A:Molecule type: mRNA

A:Residues: 1-170 <DOB>

A:Cross-references: GB:M16443; NID:G164033; PIDN:AAA30878.1; PID:G164034

R:Mitra, S.P.; Muraki, K.; Brown, D.R.; Parsons, A.M.; Carraway, R.E.

Regul. Pept. 28, 11-22, 1990

A:Title: Canine neurotensin, neurotensin(6-13) and neuromedin N: primary structures and

A:Reference number: A60319; MUID:90222594; PMID:2158127

A:Accession: B60319

A:Molecule type: protein

A:Residues: 143-148 <MIT>

A:Accession: A60319

A:Molecule type: protein

A:Residues: 152-163 <MIT>

R:Mogard, M.H.; Reeve Jr., J.R.; Shively, J.E.; Ben-Avram, C.M.; Eysselein, V.E.; Walsh,

Regul. Pept. 14, 313-321, 1986

A:Title: Isolation and characterization of a neurotensin-like decapeptide from a canine

A:Reference number: A60324; MUID:86314883; PMID:3749527

A:Accession: A60324

A:Molecule type: protein

A:Residues: 154-163 <MOG>

R:Carraway, R.E.; Mitra, S.P.

Biochem. Biophys. Res. Commun. 179, 301-308, 1991

A:Title: Purification of large neuromedin N (NMN) from canine intestine and its identifi

A:Reference number: JN0293; MUID:91354266; PMID:1863359

A:Accession: JN0293

A:Molecule type: protein

A:Residues: 24-43 <CAR>

A:Experimental source: small intestine

R:Carraway, R.E.; Mitra, S.P.

J. Biol. Chem. 265, 8627-8631, 1990

A:Title: Differential processing of neurotensin/neuromedin N precursor(s) in canine brain

A:Reference number: A36272; MUID:90256783; PMID:2341398

A:Accession: A36272

A:Molecule type: protein

A:Residues: 128-147 <CA2>

C:Superfamily: neurotensin

C:Keywords: hormone; neuropeptide; pyroglutamic acid

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-148/Product: large neuromedin N-125 #status experimental <LNM>

F:143-148/Product: neuromedin N #status experimental <NMN>

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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:14:33 ; Search time 17 Seconds
(without alignments)
470.267 Million cell updates/sec

Title: US-09-927-565A-1

Perfect score: 890

Sequence: 1 MMAGMKIQLVCMLLAFSSW.....QLYENKPRRPVILKRDYYY 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	890	100.0	170	1	NEUT_HUMAN
2	804	90.3	169	1	NEUT_BOVIN
3	794	89.2	170	1	NEUT_CANFA
4	742	83.4	169	1	NEUT_MOUSE
5	711	79.9	169	1	NEUT_RAT
6	83.5	9.4	832	1	EP2_CRYPV
7	81.5	9.2	102	1	RS10_SULTO
8	81.5	9.2	230	1	NTPD_ENTHR
9	79.5	8.9	196	1	ADEN_ADEBA
10	79.5	8.9	346	1	XYNB_THENE
11	79.5	8.9	479	1	PAP1_VACCV
12	79.5	8.9	479	1	PAP1_VARV
13	79	8.9	811	1	RPOP_NEUN
14	79	8.9	819	1	LON_CHLPN
15	79	8.9	1626	1	TP2B_HUMAN
16	78.5	8.8	416	1	PALY_VITVI
17	78.5	8.8	429	1	CGBI_MESAU
18	78.5	8.8	479	1	PAP1_VACCC
19	78	8.8	283	1	Y43C_MYCPN
20	78	8.8	908	1	RB35_METJA
21	76.5	8.6	377	1	Y835_METJA
22	75.5	8.5	401	1	PILC_PSEPU
23	75	8.4	505	1	TCMO_ZINEL
24	75	8.4	506	1	TCMO_SOYBN
25	75	8.4	1612	1	TP2B_CRILO
26	74	8.3	585	1	Y187_MYCGE
27	74	8.3	1067	1	MICA_HUMAN
28	74	8.3	1612	1	TP2B_MOUSE
29	73.5	8.3	3680	1	END_CANFA
30	73	8.2	843	1	CYAA_HAEIN
31	73	8.2	908	1	R8L4_ARATH
32	73	8.2	1939	1	MYH6_HUMAN
33	73	8.2	3433	1	UTRO_HUMAN

RESULT 1

NEUT_HUMAN
ID NEUT_HUMAN STANDARD; PRT; 170 AA.
AC P30990;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin/neuromedin N precursor [Contains: Large neuromedin N (NmN-125); Neuromedin N (NmN) (NN); Neurotensin (NT); Tail peptide].
GN NTS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98191186; PubMed=9530155;
RA Dong Z., Wang X., Zhao Q., Townsend C.M. Jr., Evers B.M.;
RT "DNA methylation contributes to expression of the human neurotensin/neuromedin N gene."
RL Am. J. Physiol. 274:G535-G543(1998).
RN [2]
RP SEQUENCE OF 1-120 FROM N.A.
RX MEDLINE=93063858; PubMed=1436492;
RA Bean A.J., Dagerlind A., Hoekfelt T., Dobner P.R.;
RT "Cloning of human neurotensin/neuromedin N genomic sequences and expression in the ventral mesencephalon of schizophrenics and age/sex matched controls."
RL Neuroscience 50:259-268(1992).
CC -!- FUNCTION: Neurotensin may play an endocrine or paracrine role in the regulation of fat metabolism. It causes contraction of smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted; Packaged within secretory vesicles.
CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.

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EMBL; U91618; AAB50564.1; -;
EMBL; S47339; AAB23934.1; -;
PIR; I58190; I58190.
DR GENE; HGNC:8038; NTS.
DR MIM; 162650; -;
GO; GO:0005625; C:soluble fraction; TAS.
KW Cleavage on pair of basic residues; Vasoactive; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 148 LARGE NEUROMEDIN N (NMN-125).
FT PEPTIDE 144 148 NEUROMEDIN N.
FT PEPTIDE 151 163 NEUROTENSIN.
FT PEPTIDE 166 170 TAIL PEPTIDE (POTENTIAL).

ALIGNMENTS

34	72	8.1	233	1	BCLX_HUMAN	Q07817	homo sapien
35	72	8.1	465	1	MYH6_RABIT	P04460	oryctolagus
36	72	8.1	505	1	TCMO_ARATH	P92994	arabidopsis
37	72	8.1	505	1	TCMO_CICAR	O81928	cicer ariet
38	72	8.1	879	1	YN65_YEAST	P42837	saccharomyc
39	72	8.1	1536	1	SIN3_YEAST	P22579	saccharomyc
40	72	8.1	2269	1	WDR9_HUMAN	Q9NS16	homo sapien
41	71.5	8.0	682	1	PAL1_POPKI	P45731	populus kit
42	71	8.0	301	1	B3G5_PANPA	Q9N294	p beta-1.3-
43	71	8.0	325	1	THIL_BACSU	O05514	bacillus su
44	71	8.0	445	1	XAV5_XANCV	P19520	xanthomonas
45	71	8.0	505	1	TCMO_POPTM	O24312	populus tre

SQ SEQUENCE 170 AA; 19795 MW; 66E2E146DA08E3C7 CRC64;

Query Match 100.0%; Score 890; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.7e-74;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMAGKIQVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAVPSWKMTLLN 60
 DB 1 MMAGKIQVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAVPSWKMTLLN 60

QY 61 VCSLVNNLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFQHW 120
 DB 61 VCSLVNNLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFQHW 120

QY 121 LIQEDILTNDKNGKEEVIRKPIYILKQLYENKPRPYILKRDSDYY 170
 DB 121 LIQEDILTNDKNGKEEVIRKPIYILKQLYENKPRPYILKRDSDYY 170

RESULT 2

NEUT_BOVIN STANDARD; PRT; 169 AA.

AC P01156;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin/neuromedin N precursor [Contains: Large neuromedin N (NmN-125); Neuromedin N (NmN) (NN); Neurotensin (NT); Tail peptide].
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88169625; PubMed=2832414;
 RA Kislaukis E., Bullock B., McNeil S., Dobner P.R.;
 RT "The rat gene encoding neurotensin and neuromedin N. Structure, tissue-specific expression, and evolution of exon sequences.";
 J. Biol. Chem. 263:4963-4968(1988).
 RN [2]
 RP SEQUENCE OF 150-162.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=75095679; PubMed=1167549;
 RA Caraway R., Leeman S.E.;
 RT "The amino acid sequence of a hypothalamic peptide, neurotensin.";
 J. Biol. Chem. 250:1907-1911(1975).
 RN [3]
 RP SYNTHESIS OF NEUROTENSIN.
 RX MEDLINE=75095679; PubMed=1112838;
 RA Caraway R., Leeman S.E.;
 RT "The synthesis of neurotensin.";
 J. Biol. Chem. 250:1912-1918(1975).
 RL J. Biol. Chem. 250:1912-1918(1975).
 CC -!- FUNCTION: Neurotensin may play an endocrine or paracrine role in the regulation of fat metabolism. It causes contraction of smooth muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted; Packaged within secretory vesicles.
 CC -!- TISSUE SPECIFICITY: Brain and gut.
 CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.

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 DR EMBL; M18621; AAA30668.1;
 KW Cleavage on pair of basic residues; Vasoactive; Signal;
 KW Pyrrolidone carboxylic acid.

FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 147 LARGE NEUROMEDIN N.
 FT PEPTIDE 142 147 NEUROMEDIN N.
 FT PEPTIDE 150 162 NEUROTENSIN.
 FT PEPTIDE 165 169 TAIL PEPTIDE (POTENTIAL).
 FT MOD RES 150 150 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 169 AA; 19712 MW; 7B78760D5E4D7D32 CRC64;

Query Match 90.3%; Score 804; DB 1; Length 169;
 Best Local Similarity 90.5%; Pred. No. 1.2e-66;
 Matches 153; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 MAGMKIQVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAVPSWKMTLLN 61
 DB 1 MAGMKIQVCMILLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAVPSWKMTLLN 60

QY 62 CSLVNNLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFQHW 121
 DB 62 CSLVNNLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFQHW 120

QY 122 IQEDILTNDKNGKEEVIRKPIYILKQLYENKPRPYILKRDSDYY 170
 DB 122 IQEDILTNDKNGKEEVIRKPIYILKQLYENKPRPYILKRDSDYY 169

RESULT 3

NEUT_CANPA STANDARD; PRT; 170 AA.

AC P10673; Q9TS28;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurotensin/neuromedin N precursor [Contains: Large neuromedin N (NmN-125); Neuromedin N (NmN) (NN); Neurotensin (NT); NT-tail; Tail peptide].
 OS Canis familiaris (Dog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 ON NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87204168; PubMed=3472221;
 RA Dobner P.R., Barber D.L., Villa-Komaroff L., McKiernan C.;
 RT "Cloning and sequence analysis of cDNA for the canine neurotensin/neuromedin N precursor.";
 Proc. Natl. Acad. Sci. U.S.A. 84:3516-3520(1987).
 RN [2]
 RP SEQUENCE OF 128-148.
 RX MEDLINE=90256783; PubMed=2341398;
 RA Caraway R.E., Mitra S.P.;
 RT "Differential processing of neurotensin/neuromedin N precursor in canine brain and intestine.";
 J. Biol. Chem. 265:8627-8631(1990).
 RN [3]
 RP SEQUENCE OF 24-43.
 RC TISSUE=Intestine;
 RX MEDLINE=91354266; PubMed=1883359;
 RA Caraway R.E., Mitra S.P.;
 RT "Purification of large neuromedin N (NMN) from canine intestine and its identification as NMN-125.";
 Biochem. Biophys. Res. Commun. 179:301-308(1991).
 RN [4]
 RP SEQUENCE OF 151-170.
 RC TISSUE=Intestine;
 RX MEDLINE=93157144; PubMed=1494486;
 RA Caraway R.E., Mitra S.P., Salmons R.;
 RT "Isolation and quantitation of several new peptides from the canine neurotensin/neuromedin N precursor.";
 Peptides 13:1039-1047(1992).
 CC -!- FUNCTION: Neurotensin may play an endocrine or paracrine role in the regulation of fat metabolism. It causes contraction of smooth muscle.

```
CC -!- SUBCELLULAR LOCATION: Secreted; Packaged within secretory
CC vesicles.
CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16443; AAA30878.1; -
DR PIR; A28035; UNDC.
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 23
FT CHAIN 24 148 LARGELY NEUROMEDIN N.
FT PEPTIDE 143 148 NEUROMEDIN N.
FT PEPTIDE 151 163 NEUROTENSIN.
FT PEPTIDE 151 170 NT-TAIL.
FT PEPTIDE 166 170 TAIL PEPTIDE (POTENTIAL).
FT MOD RES 151 151 PYROGLUTAMATE CARBOXYLIC ACID.
SQ SEQUENCE 170 AA; 19863 MW; A54700163AC54962 CRC64;

Query Match 89.2%; Score 794; DB 1; Length 170;
Best Local Similarity 90.0%; Pred. No. 1e-65;
Matches 153; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MMAGKIQVLCVLLAFSSWSLCSDESEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
Db 1 MMAGKIQVLCVLLAFSSWSLCSDESEEMKALEADFLTNMHTSKISKASVSSWKMTLLN 60
Qy 61 VCSLVNVLNSPAEETGEVHEBELVARRKLPALDGFSLSEAMLTIVQLHKICHSAFOHWE 120
Db 61 VCSFVNVLNSQAEETGEVHEBELVARRKLPALDGFSLSEAMLTIVQLHKICHSAFOHWE 120
Qy 121 LIQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRPYILKRDYSYY 170
Db 121 LIQEDVLDAGNDKNGKEVIRKIPYILKQLYENKPRPYILKRGYSYY 170

RESULT 4
NEUT MOUSE
ID NEUT MOUSE STANDARD; PRT; 169 AA.
AC Q9D3E9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin/neuromedin N precursor [Contains: Large neuromedin N (NmN-
DE 125); Neuromedin N (NmN) (NN); Neurotensin (NT); Tail peptide].
GN NTS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=129;
RA Dobner P.R., Fadel J., Deitemeyer N., Carraway R.E., Deutch A.Y.;
RT "Neurotensin-deficient mice show altered responses to antipsychotic
RT drugs";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Ahn H.-J., Cho J.-J.;
RT "Mouse proneurotensin/proneuromedin N is induced in mast cell line
RT after IGE cross-linking";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Intestine;
RC MEDLINE=21085660; PubMed=11217851;
RX
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
CC -!- FUNCTION: Neurotensin may play an endocrine or paracrine role
CC in the regulation of fat metabolism. It causes contraction of
CC smooth muscle (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; Packaged within secretory
CC vesicles (By similarity).
CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
CC -----
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CC -----
DR EMBL; AF348489; AAK28626.1; -
DR EMBL; AF304160; AAK15263.1; -
DR EMBL; AK017212; BAB30636.1; -
DR MGD; MGI:1914655; 5033428B16Rik.
KW Cleavage on pair of basic residues; Vasoactive; Signal.
FT SIGNAL 1 22
FT CHAIN 23 147 LARGELY NEUROMEDIN N.
FT PEPTIDE 142 147 NEUROMEDIN N.
FT PEPTIDE 150 162 NEUROTENSIN.
FT PEPTIDE 165 169 TAIL PEPTIDE (POTENTIAL).
SQ SEQUENCE 169 AA; 19607 MW; D153319F5F0925DC CRC64;

Query Match 83.4%; Score 742; DB 1; Length 169;
Best Local Similarity 81.7%; Pred. No. 5.6e-61;
Matches 138; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 2 MMAGKIQVLCVLLAFSSWSLCSDESEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 61
Db 1 MRGMNLQVLCVLLAFSSWSLCSDESEEDVRALEADLTNNMHTSKISKASPPSWKMTLLN 60
Qy 62 CSLVNNVLNSPAEETGEVHEBELVARRKLPALDGFSLSEAMLTIVQLHKICHSAFOHWE 121
Db 61 CSLVNNVLNSPAEETGEVHEBELVARRKLPALDGFSLSEAMLTIVQLHKICHSAFOHWE 120
Qy 122 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRPYILKRDYSYY 170
Db 121 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRPYILKRGYSYY 169

RESULT 5
NEUT RAT
ID NEUT RAT STANDARD; PRT; 169 AA.
AC P20058; Q9QV80;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotensin/neuromedin N precursor [Contains: Large neuromedin N (NmN-
DE 125); Neuromedin N (NmN) (NN); Neurotensin (NT); Tail peptide].
```

NTS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88169625; PubMed=2832414;
RA Kilauea E., Bullock B., McNeil S., Dobner P.R.;
RT "The rat gene encoding neurotensin and neuromedin N. Structure,
RT tissue-specific expression, and evolution of exon sequences.";
RL J. Biol. Chem. 263:4963-4968(1988).
RN [2]
RN SEQUENCE OF 23-42, AND PROCESSING.
RX MEDLINE=93228610; PubMed=8471039;
RA Bidard J.-N., de Nadai F., Rovere C., Moinier D., Laur J.,
RA Martinez J., Cuber J.-C., Kitabgi P.;
RT "Immunological and biochemical characterization of processing products
RT from the neurotensin/neuromedin N precursor in the rat medullary
RL thymoid carcinoma 6-23 cell line.";
RL Biochem. J. 291:225-233(1993).
RN [3]
RN PROCESSING.
RX MEDLINE=93215530; PubMed=8462460;
RA de Nadai F., Rovere C., Bidard J.-N., Laur J., Martinez J.,
RA Cuber J.-C., Kitabgi P.;
RT "Biosynthesis and posttranslational processing of the
RT neurotensin/neuromedin N precursor in the rat medullary thymoid
RL carcinoma 6-23 cell line. Effect of dexamethasone.";
RL Endocrinology 132:1614-1620(1993).
CC -!- FUNCTION: Neurotensin may play an endocrine or paracrine role
CC in the regulation of fat metabolism. It causes contraction of
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted; Packaged within secretory
CC vesicles.
CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
CC
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CC
CC EMBL; M21187; AAA41712.1; ALT_INIT.
DR EMBL; M21218; AAA41712.1; JOINED.
DR PIR; A28146; A28146.
KW Cleavage on pair of basic residues; Vasoactive; Signal.
FT SIGNAL 1 22
FT CHAIN 23 147 LARGE NEUROMEDIN N.
FT PEPTIDE 142 147 NEUROMEDIN N.
FT PEPTIDE 150 162 NEUROTENSIN.
FT PEPTIDE 165 169 TAIL PEPTIDE (POTENTIAL).
SQ SEQUENCE 169 AA; 19563 MW; 91CF0CF68C3D3C91 CRC64;
Query Match 79.9%; Score 711; DB 1; Length 169;
Best Local Similarity 78.1%; Pred. No. 3.8e-58;
Matches 132; Conservative 17; Mismatches 20; Indels 0; Gaps 0;
QY 2 MAGMKIQLVCMALLAFSSWSLCSSEEMKALEADFLTNMHTSKSKAHVPSPKMTLLNV 61
DB 1 MIGNNLQVLCITLAFSSWSLCSSEEDVRALEADLLTNMASKVSKSPSPKMTLLNV 60
QY 62 CSLVNNLNSPAETGEVHEELVARRKLPALTADGFSLEAMLTIVQLHKICHSRAFOHWEL 121
DB 61 CSLINNLSAAEEAGEMRDDDLVAKRKLPLVLDLDFSLLEALLTVFLQKICHSRAFOHWEL 120
QY 122 IOEDILDGNDKNGKEEVKIPILKQLYENKPRPYILKRDSYYY 170
DB 121 IOEDILDGNDKNGKEEVKIPILKQLYENKPRPYILKRDSYYY 169

RESULT 6
EF2_CRYPV STANDARD; PRT; 832 AA.
AC Q23716;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 2 (EF-2).
OS Cryptosporidium parvum
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_taxid=5807;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=AUCP-1;
RX MEDLINE=95356792; PubMed=7630379;
RA Jones D.E., Tu T.D., Mathur S., Sweeney R.W., Clark D.P.;
RT "Molecular cloning and characterization of a Cryptosporidium parvum
RT elongation factor-2 gene.";
RL Mol. Biochem. Parasitol. 71:143-147(1995).
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC
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CC
CC EMBL; U21667; AAC46607.1;
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EF_G.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_Gtp.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFT.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFACITOR_GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding; Phosphorylation.
FT NP_BIND 26 33 GTP (BY SIMILARITY).
FT NP_BIND 98 102 GTP (BY SIMILARITY).
FT NP_BIND 152 155 GTP (BY SIMILARITY).
FT MOD_RES 57 57 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 59 59 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 689 689 DIPHTHAMIDE (BY SIMILARITY).
SQ SEQUENCE 832 AA; 92761 MW; 577D2DE3D77E3FA CRC64;
Query Match 9.4%; Score 83.5; DB 1; Length 832;
Best Local Similarity 24.7%; Pred. No. 6.4;
Matches 40; Conservative 19; Mismatches 54; Indels 49; Gaps 9;
QY 22 LCSDESEEMKALEADFL-TNMHTSKSKAH---VPSMKWT-----LLAVCSLVN 66
DB 666 LC-----EEDMGIRFNLDVTLHADAIHRGAGQITPTCRRVYAAALFASPLLEPMFLV- 721
QY 67 NLNSPASETEGEV-----HEE-----ELVARRKLPALTADGFSLEAMLTIVQLH 108
DB 722 EISAPQEVGGIYATLNQRCHVHEEPKSTPQVEIKAYLPVA-DSEKFTTVLRAATSG 780
QY 109 KICHSRAFOHWELIOEDILDGND-----KNGKEEV 139
DB 781 KAPPCQCVDFHWELINGDPLEKGSKTEELVKAIRRRKNKEI 822

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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:14:08 ; Search time 41 Seconds
(without alignments)
658.135 Million cell updates/sec

Title: US-09-927-565A-1
Perfect score: 890
Sequence: 1 MMAGMKIQLVCMLLAFSSW.....QLYENKPRPYILKRDSTYY 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A. Geneseq 19Jun03.*

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- 5: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT.*
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- 21: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	890	100.0	170	22 AAU08929	Human preproneurot
2	890	100.0	170	24 ABUS56410	Lung cancer-associ
3	890	100.0	170	24 ABUS56659	Lung cancer-associ
4	664	74.6	129	21 AAG00256	Human secreted pro
5	90	10.1	279	21 AAB29865	Human secreted pro
6	87.5	9.8	322	20 AAY19902	B. burgdorferi ant
7	80	9.0	424	20 AAY34627	Chlamydia pneumoni
8	80	9.0	841	22 ABG13829	Novel human diagno
9	79.5	8.9	652	18 AAW18010	Plasmodium falcipa

10	79	8.9	400	22	ABG02720	Novel human diagno
11	79	8.9	1139	22	ABG22397	Novel human diagno
12	79	8.9	1621	22	AAW25646	Human protein sequ
13	78.5	8.8	550	20	AAW02299	Computer generated
14	78.5	8.8	550	20	AAW02300	Computer generated
15	78.5	8.8	550	20	AAW02302	Computer generated
16	78.5	8.8	550	20	AAW02303	Computer generated
17	78.5	8.8	550	20	AAW02304	Computer generated
18	78.5	8.8	550	20	AAW02307	Computer generated
19	78.5	8.8	550	20	AAW02390	A (E)-beta-farnese
20	78.5	8.8	550	21	AAW02290	Mint E-b-farnesene
21	77.5	8.7	1726	24	AAO16416	Human nucleic acid
22	77.5	8.7	2816	22	AAU68572	Human novel cytoki
23	76.5	8.6	216	23	ABP53327	Crassula barkleyi
24	76.5	8.6	223	21	AAW08259	Arabidopsis thalia
25	76.5	8.6	247	21	AAW08258	Arabidopsis thalia
26	76.5	8.6	273	21	AAW08257	Arabidopsis thalia
27	76.5	8.6	550	20	AAW02306	Computer generated
28	76	8.5	428	24	ABU11835	Human MDT polypep
29	75.5	8.5	491	24	ABJ25609	Aspergillus fumiga
30	75.5	8.5	554	24	ABJ26209	Aspergillus fumiga
31	75.5	8.5	2485	21	AAJ18172	Plasmodium falcipa
32	75	8.4	212	22	AAW44285	Mutant bcl-Xl prot
33	75	8.4	233	21	AAW83223	Bcl-x polypeptide.
34	75	8.4	233	21	AAW69969	Human Bcl-XL prote
35	75	8.4	233	22	AAW44262	Human Bcl-XL prote
36	75	8.4	233	22	AAW50538	Human Bcl-XL prote
37	75	8.4	233	22	AAW47515	Protein encoded by
38	75	8.4	237	23	ABW78480	Wild type BclXl pr
39	75	8.4	411	22	AAU00219	Bcl-Xl-BTR apoptos
40	75	8.4	419	21	AAW22185	Arabidopsis thalia
41	75	8.4	419	21	AAW48520	Arabidopsis thalia
42	75	8.4	485	22	AAU00222	Lfn-Bcl-XL apoptos
43	75	8.4	565	21	AAW22184	Arabidopsis thalia
44	75	8.4	565	21	AAW48519	Arabidopsis thalia
45	75	8.4	602	21	AAW22183	Arabidopsis thalia

ALIGNMENTS

- RESULT 1
AAU08929
ID AAU08929 standard; Protein, 170 AA.
XX AAU08929;
AC AAU08929;
XX
DT 18-DEC-2001 (first entry)
XX Human preproneurotensin/neuromedin N.
DE
XX Human; neurotensin; neuromedin N; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; anticonvulsant; antidepressant;
KW antithyroid; cytostatic; antiarteriosclerotic; hepatotrophic;
KW antiinflammatory; cell proliferative disorder; neurological disorder;
KW endocrine disorders; gene therapy; antineoplastic therapy; HspN;
KW Alzheimer's disease; anyotrophic lateral sclerosis; depression;
KW diabetic neuropathy; epilepsy; Down's syndrome; Huntington's disease;
KW Parkinson's disease; Cushing's disease; diabetes insipidus;
KW diabetes mellitus; hypoglycaemia; hypoglycaemia; goitre;
KW arteriosclerosis; atherosclerosis; hepatitis; cancer; leukaemia;
KW INCYTE2923961; INCYTE1576389; INCYTE1309070.

OS	Homo sapiens.				
XX	Key	Location/Qualifiers			
XX	Peptide	1..142			
FT	Peptide	/label= Prepro_peptide			
FT	Peptide	127..136			
FT	Peptide	/note= Unknown			
FT	Peptide	/claim 1"			
FT	Peptide	143..148			

FT Peptide /label= Neurotensin
 FT 151...163
 XX /label= Neuromedin_N
 PN US6274720-B1.
 PD 14-AUG-2001.
 XX
 PF 31-DEC-1997; 97US-0002114.
 XX
 PR 31-DEC-1997; 97US-0002114.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal P, Shah P, Corley NC;
 XX WPI; 2001-588905/66.
 DR N-PSDB; AAS13802.
 XX
 XX Isolated polynucleotide encoding human preneurotensin/neuromedin N
 PT is used in the diagnosis, treatment and prevention of cell
 PT proliferative, neurological and endocrine disorders -
 XX
 PS Claim 1; Fig 1; 27pp; English.
 XX
 CC The invention relates to an isolated polynucleotide sequence encoding
 CC human neurotensin/neuromedin N (HPPN) neuropeptides. HPPN polynucleotides
 CC may be used for the diagnosis, treatment and prevention of cell
 CC proliferative, neurological and endocrine disorders, as well as in gene
 CC therapy, antisense therapy to block transcription of the mRNA encoding
 CC HPPN. HPPN polynucleotides may be used to generate hybridisation probes
 CC useful for mapping the gene. HPPN may be used to treat or prevent a
 CC neurological disorder comprising Alzheimer's disease, amyotrophic lateral
 CC sclerosis, depression, diabetic neuropathy, epilepsy, Down's syndrome,
 CC Huntington's disease and Parkinson's disease, an endocrine disorder
 CC comprising Cushing's disease, diabetes insipidus, diabetes mellitus,
 CC hyper- and hypoglycaemia and goitre. Agonists of HPPN may also be used to
 CC treat or prevent the above mentioned disorders, whereas an antagonist
 CC of HPPN may be used to treat or prevent a cell proliferative disorder
 CC comprising arteriosclerosis, atherosclerosis, hepatitis and cancer
 CC including leukaemia. Antibodies specific for HPPN may be used for the
 CC diagnosis of the disorders or in an assay to monitor patients being
 CC treated with HPPN or agonists, antagonists, and inhibitors of HPPN.
 CC The present sequence represents HPPN and is encoded by a cDNA derived
 CC from overlapping Incyte clones 292396L, 1576389 and 1309070.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 890; DB 22; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMAGMKIQLVCMMLLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
 DB 1 MMAGMKIQLVCMMLLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
 QY 61 VCSLVNINLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFAQHWE 120
 DB 61 VCSLVNINLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFAQHWE 120
 QY 121 LIQEDILTGTNDKNGKEEVIRKIPYILKQLYENKPRRPYILKRDSYYY 170
 DB 121 LIQEDILTGTNDKNGKEEVIRKIPYILKQLYENKPRRPYILKRDSYYY 170
 RESULT 2
 ABUS6410
 ID ABUS6410 standard; Protein; 170 AA.
 XX
 AC ABUS6410;
 XX
 DT 02-APR-2003 (first entry)
 XX

DE Lung cancer-associated polypeptide #3.
 XX
 KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN WO200286443-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US12476.
 XX
 PR 18-APR-2001; 2001US-284770P.
 PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.
 PR 12-APR-2002; 2002US-372248P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76126.
 XX
 CC Detecting a lung cancer-associated transcript in a cell from a patient
 CC for treating lung cancer, by contacting a biological sample from the
 CC patient with a polynucleotide that exhibits increased or decreased
 CC expression in lung cancer -
 XX
 PS Claim 27; Page 190; 453pp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
 CC polypeptides of the invention.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 890; DB 24; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1e-86;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMAGMKIQLVCMMLLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
 DB 1 MMAGMKIQLVCMMLLAFSSWSLCSSEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
 QY 61 VCSLVNINLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFAQHWE 120
 DB 61 VCSLVNINLNSPAEETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFAQHWE 120
 QY 121 LIQEDILTGTNDKNGKEEVIRKIPYILKQLYENKPRRPYILKRDSYYY 170
 XX

Qy 61 VCSLVNLSNLSPAETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFOHWE 120
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 Db 61 VCSLVNLSNLSPAETGEVHEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSAFOHWE 120
 |||||
 Qy 121 LIQEDILDT 129
 |||||
 Db 121 LIQEDILDT 129
 |||||

RESULT 5
 AAB29865
 ID AAB29865 standard; Protein; 279 AA.
 XX
 AC AAB29865;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Human secreted protein BLAST search protein SEQ ID NO: 123.
 XX
 DE Cytostatic; immunosuppressive; neutropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200061779-A1.
 XX
 PD 19-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US09068.
 PF
 XX 09-APR-1999; 99US-0128699.
 PR
 PR 20-JAN-2000; 2000US-0177050.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-647424/62.
 XX
 XX Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 PT
 XX Disclosure; Page 457-458; 495pp; English.

XX The invention relates to the isolation of genes AAC63410-C63458 encoding
 CC the human secreted proteins AAB29802-B29850. This sequence represents a
 CC peptide fragment homologous to the protein encoded by the gene given
 CC in the descriptor line. The sequence is a search result from a BLASTX
 CC homology search. The genes and proteins are useful for preventing,
 CC ameliorating or treating medical conditions, e.g. by protein or gene
 CC therapy. The genes are isolated from a range of human tissues disclosed
 CC in the specification. The nucleic acids, proteins, antibodies and
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
 CC (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such
 CC as myocardial ischaemia; (d) wound healing; (e) neurological diseases
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
 CC as viral, bacterial, fungal and parasitic infections.
 XX
 XX Sequence 279 AA;

Query Match 10.1%; Score 90; DB 21; Length 279;
 Best Local Similarity 22.2%; Pred. NO. 0.42;
 Matches 24; Conservative 28; Mismatches 44; Indels 12; Gaps 3;

Qy 26 SEEMKALEADFLTNMHTSKISKARV-----PSWKMTLLNVCSLVNLSNLSPAETGEVH 79
 |||||
 Db 165 SEGKSNIMPADLVLPQPSQVNSLEVITPETAETWRCVLTACKSLSHSI---GQSLQVW 221
 |||||
 Qy 80 EEEELVARRKLPALDGFSLSEAMLTIIYQLHKICHSR---AFOHWELIQE 124
 |||||
 Db 222 ENDLVAARQTRDSIGSQDLSRLLTWARMMSVSYGETTILSLHWMQVLE 269
 |||||

RESULT 6
 AAY19902
 ID AAY19902 standard; Protein; 322 AA.
 XX
 AC AAY19902;
 XX
 DT 19-JUL-1999 (first entry)
 XX
 DE B. burgdorferi antigenic protein, f210.aa.
 XX
 DE Antigenic protein; vaccine; Lyme disease; infection; detection.
 KW
 XX Borrelia burgdorferi.
 OS
 XX WO9859071-A1.
 PN
 XX 30-DEC-1998.
 PD
 XX 18-JUN-1998; 98WO-US12718.
 PF
 XX 03-SEP-1997; 97US-0057483.
 PR
 PR 20-JUN-1997; 97US-0050359.
 PR
 PR 22-JUL-1997; 97US-0053344.
 PR
 PR 22-JUL-1997; 97US-0053377.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PA (MEDI-) MEDIMMUNE INC.
 XX
 XX Choi GH, Erwin AL, Hanson MS, Lathigra R;
 PI
 XX WPI; 1999-189980/16.
 DR
 DR N-PSDB; AAX61599.
 XX
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop
 PT products for the diagnosis, prevention and treatment of diseases
 PT caused by Borrelia, particularly Lyme disease
 XX
 XX Claim 12; Page 112; 275pp; English.

XX This sequence represents a Borrelia burgdorferi (Bb) protein of the
 CC invention, which is suitable for use in a vaccine. The Bb polypeptides
 CC can be used in vaccines for eliciting protective antibodies to members of
 CC the Borrelia genus, particularly for the use against Lyme disease in
 CC humans and animals. They can be used for preventing or attenuating an
 CC infection caused by a member of the Borrelia genus. The products can also
 CC be used for detection of members of the Borrelia genus.

XX Sequence 322 AA;

Query Match 9.8%; Score 87.5; DB 20; Length 322;
 Best Local Similarity 25.9%; Pred. No. 0.95;
 Matches 44; Conservative 32; Mismatches 55; Indels 39; Gaps 9;

Qy 5 MKIOLVCMLLIAPS-----SWSLCSDSSEEMK-----ALEADFLTNMHTSKISKA 49
 |||||
 Db 1 MKIITIMLLALLDFPLNARLLDISIKRADEIKYSSVNLILEKEYTTFPTSEIK- 59
 |||||
 Qy 50 HVPKMKMTLLNVCSLVN-----LNSPAETGE-VHEEELVARRKLPALDGFSLSEAML 102
 |||||
 Db 60 --NIYKUTEHFVKSIMLNKNTYSLNSNYKEANKYLQSELDKRLKYK--FKIKIN 115
 |||||
 Qy 103 TIYQLHKICHRS-RAFOHWELIQEDILDTGNDKNGKE--EVIKRKIPYILK 149
 |||||
 Db 116 GIFKSHSLIYTKGFGYKLELYIE-----NNAEPLKIFNLNITYFLK 156
 |||||

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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:16:39 ; Search time 21 Seconds
(without alignments)
342.516 Million cell updates/sec

Title: US-09-927-565A-1

Perfect score: 890

Sequence: 1 MMAGKTKQLVCMLLAFSSW.....QLYENKPRPYLKRDYYY 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	890	100.0	170	3 US-09-002-114-1	Sequence 1, Appl
2	804	90.3	169	3 US-09-002-114-3	Sequence 3, Appl
3	711	79.9	169	3 US-09-002-114-4	Sequence 4, Appl
4	80.5	9.0	550	3 US-09-166-460-13	Sequence 13, Appl
5	80.5	9.0	550	3 US-09-361-718-13	Sequence 13, Appl
6	80	9.0	424	4 US-09-198-452A-45	Sequence 45, Appl
7	79.5	8.9	652	4 US-08-559-896B-2	Sequence 2, Appl
8	78.5	8.8	550	3 US-09-166-460-2	Sequence 2, Appl
9	78.5	8.8	550	3 US-09-166-460-5	Sequence 5, Appl
10	78.5	8.8	550	3 US-09-166-460-7	Sequence 7, Appl
11	78.5	8.8	550	3 US-09-166-460-9	Sequence 9, Appl
12	78.5	8.8	550	3 US-09-166-460-11	Sequence 11, Appl
13	78.5	8.8	550	3 US-09-166-460-15	Sequence 15, Appl
14	78.5	8.8	550	3 US-09-166-460-17	Sequence 17, Appl
15	78.5	8.8	550	3 US-09-166-460-19	Sequence 19, Appl
16	78.5	8.8	550	3 US-09-166-460-20	Sequence 20, Appl
17	78.5	8.8	550	3 US-09-166-460-21	Sequence 21, Appl
18	78.5	8.8	550	3 US-09-166-460-23	Sequence 23, Appl
19	78.5	8.8	550	3 US-09-166-460-24	Sequence 24, Appl
20	78.5	8.8	550	3 US-09-166-460-25	Sequence 25, Appl
21	78.5	8.8	550	3 US-09-166-460-28	Sequence 28, Appl
22	78.5	8.8	550	3 US-09-361-718-2	Sequence 2, Appl
23	78.5	8.8	550	3 US-09-361-718-5	Sequence 5, Appl
24	78.5	8.8	550	3 US-09-361-718-9	Sequence 9, Appl
25	78.5	8.8	550	3 US-09-361-718-11	Sequence 11, Appl
26	78.5	8.8	550	3 US-09-361-718-15	Sequence 15, Appl
27	78.5	8.8	550	3 US-09-361-718-15	Sequence 15, Appl

28 78.5 8.8 550 3 US-09-361-718-17 Sequence 17, Appl
29 78.5 8.8 550 3 US-09-361-718-19 Sequence 19, Appl
30 78.5 8.8 550 3 US-09-361-718-20 Sequence 20, Appl
31 78.5 8.8 550 3 US-09-361-718-21 Sequence 21, Appl
32 78.5 8.8 550 3 US-09-361-718-23 Sequence 23, Appl
33 78.5 8.8 550 3 US-09-361-718-24 Sequence 24, Appl
34 78.5 8.8 550 3 US-09-361-718-25 Sequence 25, Appl
35 78.5 8.8 550 3 US-09-361-718-28 Sequence 28, Appl
36 78.5 8.8 550 4 US-09-398-395A-28 Sequence 28, Appl
37 78.5 8.8 550 4 US-09-887-586A-28 Sequence 28, Appl
38 78.5 8.8 550 4 US-09-895-752-28 Sequence 28, Appl
39 78.5 8.8 550 4 US-09-903-012B-28 Sequence 28, Appl
40 76.5 8.6 550 3 US-09-166-460-27 Sequence 27, Appl
41 76.5 8.6 550 3 US-09-361-718-27 Sequence 27, Appl
42 75 8.4 233 1 US-08-081-448-6 Sequence 6, Appl
43 75 8.4 233 1 US-08-607-269-24 Sequence 24, Appl
44 75 8.4 233 2 US-08-470-670A-7 Sequence 7, Appl
45 75 8.4 233 3 US-08-167-921-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-002-114-1
; Sequence 1, Application US/09002114
; Patent No. 6274720
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/002,114
; APPLICATION NUMBER: US/09/002,114
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0450 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PITUNOT03
; CLONE: 1760566
; US-09-002-114-1
Query Match 100.0%; Score 890; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e-95;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMAGMKIQLVCMILLAFSSWSLCSDEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60
DB 1 MMAGMKIQLVCMILLAFSSWSLCSDEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 60

QY 61 VCSLVNLSNLSPAEETGEVHEELVARRKLPALDGFSLAEMLTYYQLHKICHSAFQHWEL 120
DB 61 VCSLVNLSNLSPAEETGEVHEELVARRKLPALDGFSLAEMLTYYQLHKICHSAFQHWEL 120

QY 121 LIQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 170
DB 121 LIQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 170

RESULT 2
US-09-002-114-3
; Sequence 3, Application US/09002114
; Patent No. 6274720
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,114
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0450 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 163424
US-09-002-114-3
Query Match 90.3%; Score 804; DB 3; Length 169;
Best Local Similarity 90.5%; Pred. No. 1e-85;
Matches 153; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 MMAGMKIQLVCMILLAFSSWSLCSDEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 61
DB 1 MMAGMKIQLVCMILLAFSSWSLCSDEEMKALEADFLTNMHTSKISKASVPSWKMTLLN 60

QY 62 VCSLVNLSNLSPAEETGEVHEELVARRKLPALDGFSLAEMLTYYQLHKICHSAFQHWEL 121
DB 62 VCSLVNLSNLSPAEETGEVHEELVARRKLPALDGFSLAEMLTYYQLHKICHSAFQHWEL 121

DB 61 CSLINNLSQAETGEFHEELITRRKPPALDGFSLAEMLTYYQLKICHSAFQHWEL 120

QY 122 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 170
DB 121 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 169

RESULT 3
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; Sequence 4, Application US/09002114
; Patent No. 6274720
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,114
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0450 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 92546
US-09-002-114-4
Query Match 79.9%; Score 711; DB 3; Length 169;
Best Local Similarity 78.1%; Pred. No. 6.9e-75;
Matches 132; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 2 MMAGMKIQLVCMILLAFSSWSLCSDEEMKALEADFLTNMHTSKISKAHVPSWKMTLLN 61
DB 1 MIGNMLQVCLTLAFSSWSLCSDEEDVRALEADLLTNMHASKVSKGSPSPSKMTLLN 60

QY 62 VCSLVNLSNLSPAEETGEVHEELVARRKLPALDGFSLAEMLTYYQLHKICHSAFQHWEL 121
DB 61 CSLINNLSNLSQAETGEFHEELITRRKPPALDGFSLAEMLTYYQLKICHSAFQHWEL 120

QY 122 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 170
DB 121 IQEDILDTGNDKNGKEVIRKIPYILKQLYENKPRRPYILKRDSSYY 169

RESULT 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:17:34 ; Search time 32 Seconds
(without alignments)

1057.280 Million cell updates/sec

Title: US-09-927-565A-1

Perfect score: 890

Sequence: 1 MMAGMKIQLVCMLLAFSSW.....QLYENKPRRPYILKRDSSYY 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:

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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	890	100.0	170	12	US-10-241-220-111
2	890	100.0	170	12	Sequence 111, App
3	82	9.2	400	12	Sequence 316, App
4	80.5	9.0	403	12	Sequence 18274, A
5	80.5	9.0	550	12	Sequence 20145, A
6	79.5	8.9	652	9	Sequence 13, Appl
7	78.5	8.8	550	9	Sequence 2, Appl
8	78.5	8.8	550	9	Sequence 28, Appl
9	78.5	8.8	550	11	Sequence 28, Appl
10	78.5	8.8	550	12	Sequence 28, Appl
11	78.5	8.8	550	12	Sequence 2, Appl
12	78.5	8.8	550	12	Sequence 5, Appl
13	78.5	8.8	550	12	Sequence 7, Appl
14	78.5	8.8	550	12	Sequence 9, Appl
15	78.5	8.8	550	12	Sequence 11, Appl
					Sequence 15, Appl

16	78.5	8.8	550	12	US-09-860-282A-17	Sequence 17, Appl
17	78.5	8.8	550	12	US-09-860-282A-19	Sequence 19, Appl
18	78.5	8.8	550	12	US-09-860-282A-20	Sequence 20, Appl
19	78.5	8.8	550	12	US-09-860-282A-21	Sequence 21, Appl
20	78.5	8.8	550	12	US-09-860-282A-23	Sequence 23, Appl
21	78.5	8.8	550	12	US-09-860-282A-24	Sequence 24, Appl
22	78.5	8.8	550	12	US-09-860-282A-25	Sequence 25, Appl
23	78.5	8.8	550	12	US-09-860-282A-28	Sequence 28, Appl
24	76.5	8.6	216	12	US-10-056-479A-1	Sequence 1, Appl
25	76.5	8.6	550	12	US-09-860-282A-27	Sequence 27, Appl
26	75.5	8.5	491	15	US-10-128-714-3267	Sequence 3267, Ap
27	75.5	8.5	554	15	US-10-128-714-8267	Sequence 8267, Ap
28	75	8.4	212	12	US-10-169-223-14	Sequence 14, Appl
29	75	8.4	233	9	US-09-734-846-2	Sequence 2, Appl
30	75	8.4	233	10	US-09-952-278-6	Sequence 6, Appl
31	75	8.4	233	12	US-10-169-223-10	Sequence 10, Appl
32	75	8.4	233	12	US-10-302-262-2	Sequence 2, Appl
33	75	8.4	233	12	US-10-116-275-171	Sequence 171, App
34	75	8.4	233	15	US-10-072-830-4	Sequence 4, Appl
35	75	8.4	850	14	US-10-029-180-96	Sequence 96, Appl
36	75	8.4	1097	12	US-10-032-585-7036	Sequence 7036, Ap
37	74.5	8.4	550	12	US-09-860-282A-22	Sequence 22, Appl
38	74	8.3	405	15	US-10-106-698-6333	Sequence 6333, Ap
39	74	8.3	662	9	US-09-799-777-53	Sequence 53, Appl
40	74	8.3	671	12	US-10-311-626-5	Sequence 5, Appl
41	73.5	8.3	1038	12	US-10-032-585-7776	Sequence 7776, Ap
42	73	8.2	552	10	US-09-961-721-2	Sequence 2, Appl
43	73	8.2	552	12	US-10-170-789-43	Sequence 43, Appl
44	72.5	8.1	235	12	US-10-369-493-11220	Sequence 11220, A
45	72.5	8.1	461	15	US-10-234-432-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-241-220-111
; Sequence 111, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241.220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 111
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-111

Query Match 100.0%; Score 890; DB 12; Length 170;
Best Local Similarity 100.0%; Pred. No. 4e-90;
Matches: 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMAGMKIQLVCMLLAFSSWSLCSDSSEEMKALBDFLTNNHTSKISKAHVPSWMTLLN	60
Db	1	MMAGMKIQLVCMLLAFSSWSLCSDSSEEMKALBDFLTNNHTSKISKAHVPSWMTLLN	60
Qy	61	VCSLVNNLNSPAETGVEVHEELVARBKLPALDGFSLSEAMLTLYQLHKICHSAFOHWE	120
Db	61	VCSLVNNLNSPAETGVEVHEELVARBKLPALDGFSLSEAMLTLYQLHKICHSAFOHWE	120
Qy	121	LIQEDILTGDNGKNGKEVIKPKIPYILKRLQYENKPRRPYILKRDSSYY	170

Db 121 LIQEDILDTGNDKNGKEVIRKIPYILKRLQYENKPRPYILKEDSYYY 170

RESULT 2

US-10-295-027-316
; Sequence 316, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynn, Richard

; APPLICANT: Hevezi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIOR FILING DATE: 2001-11-13

; PRIOR FILING DATE: 2001-11-13

; PRIOR FILING DATE: 2001-11-13

; PRIOR FILING DATE: 2001-11-13

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; PRIOR FILING DATE: 2001-11-13

; PRIOR FILING DATE: 2001-11-13

RESULT 3

US-10-369-493-18274

; Sequence 18274, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 18274

; LENGTH: 400

; TYPE: PRT

; ORGANISM: Thermoplasma acidophilum

US-10-369-493-18274

Query Match 9.2%; Score 82; DB 12; Length 400;

Best Local Similarity 27.5%; Pred. No. 2;

Matches 33; Conservative 20; Mismatches 43; Indels 24; Gaps 6;

Qy 70 SPAETGEVHEELVARRKLPALDGFSLKAMLTLYQLHKICHSR-----AFQHWELIQ 123

Db 155 SPAPSAGKA--EAVHTAPQIPAKPAGRGREILEMHGRLRRIFDKMTKAKQIMPHFTVME 212

Qy 124 E-----DILDTGNDKNGKEEV---IKRKIPYILKROLVEN---KPRRPYILKRDSSYY 169

Db 213 EVDVTSVMSILDSAKARNKVTVTGFLARIVPSILKQYPLNLYDETRVYILKK--YY 270

RESULT 4

US-10-369-493-20145

; Sequence 20145, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 20145

; LENGTH: 403

; TYPE: PRT

; ORGANISM: No. US20030233675A1loc punctiforme

US-10-369-493-20145

Query Match 9.0%; Score 80.5; DB 12; Length 403;

Best Local Similarity 26.1%; Pred. No. 3;

Matches 36; Conservative 19; Mismatches 50; Indels 33; Gaps 7;

Qy 48 KAHVPSPKMTLLNVCSLVNLLNSPAEET--GEVHEELVAR---RKLPALDGFSLKAML 102

Db 137 KVQRFGLDTIAQDIALIQGIADLVARTEFGQTYEIKSIAEFTKALEAELD-FTRFAGF 195

Qy 103 TIYQLHKICHSAFQ-----HWELIQDIL-----DTGNDKNGKEEVI 140

Db 196 TDQURRLSKSRWFDPTQIVVAEINWELTTEKLLVMEWLDGVFLSADLNNNNNGKPAV 255

Qy 141 KRK-IPYILKR-----QLY 153

Db 256 ERKEITLLFRVFFQQLY 273

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 17:15:23 ; Search time 34 Seconds
(without alignments)
1290.263 Million cell updates/sec

Title: US-09-927-565A-1
Perfect score: 890
Sequence: 1 MMAGMKIQLVCMLLAFSSW.....QLYENKPRPYILKRDSYY 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriaph:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	91.5	10.3	832	17 Q8PUW8	Q8PUW8 methanosarc
2	90	10.1	550	10 Q22880	Q22880 arabidopsis
3	87.5	9.8	171	16 O51616	O51616 borrelia bu
4	86.5	9.7	499	16 O67377	O67377 aquifex aeo
5	86.5	9.7	605	12 Q9WT50	Q9WT50 human herpe
6	86.5	9.7	610	12 Q9Q349	Q9Q349 human herpe
7	84.5	9.5	651	16 Q8NV84	Q8NV84 staphylococ
8	84.5	9.5	979	5 Q95X88	Q95X88 caenorhabdi
9	84.5	9.5	1251	5 O16637	O16637 caenorhabdi
10	84	9.4	673	16 Q8EB90	Q8EB90 shewanella
11	82	9.2	400	17 Q9HIA5	Q9HIA5 thermoplas
12	82	9.2	805	16 Q8R8R1	Q8R8R1 thermoplas
13	81.5	9.2	652	5 Q9U0D4	Q9U0D4 plasmodium
14	81.5	9.2	1964	5 Q8IIX6	Q8IIX6 plasmodium
15	81	9.1	475	17 Q8U2Y3	Q8U2Y3 pyrococcus
16	81	9.1	510	10 Q9LJY7	Q9LJY7 arabidopsis

17	80	9.0	1229	16 Q8DTJ6	Q8dtj6 streptococ
18	79.5	8.9	479	12 Q8Q667	Q8q667 camelpox vi
19	79.5	8.9	479	12 Q8V2W4	Q8v2w4 camelpox vi
20	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
21	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
22	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
23	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
24	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
25	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
26	79.5	8.9	479	12 Q8V530	Q8v530 monkeypox v
27	79	8.9	229	10 Q9LSQ8	Q9lsq8 arabidopsis
28	79	8.9	741	11 Q8C0X0	Q8c0x0 mus musculu
29	79	8.9	9271	5 Q8IES7	Q8ies7 plasmodium
30	78.5	8.8	312	13 Q9DGH8	Q9dgh8 gallus gall
31	78.5	8.8	479	12 Q9PXS1	Q9pxs1 variola vir
32	78.5	8.8	550	10 Q48935	Q48935 mentha pipe
33	78.5	8.8	913	11 Q9CYM1	Q9cym1 mus musculu
34	78	8.8	227	16 Q8FEL7	Q8fel7 corynebacte
35	78	8.8	421	5 Q8IHZ7	Q8ihz7 plasmodium
36	78	8.8	537	6 Q29016	Q29016 sus scrofa
37	78	8.8	837	10 Q9LZC7	Q9lzc7 arabidopsis
38	78	8.8	896	10 Q9FEN1	Q9fen1 arabidopsis
39	78	8.8	908	10 Q8W4J9	Q8w4j9 arabidopsis
40	78	8.8	908	10 Q9ZSY3	Q9zsy3 arabidopsis
41	78	8.8	1849	5 Q8I3L3	Q8i3l3 plasmodium
42	77.5	8.7	270	2 Q9EU59	Q9eu59 chlamydia t
43	77.5	8.7	654	4 Q8WX71	Q8wx71 homo sapien
44	77.5	8.7	1793	4 Q8TEP3	Q8tep3 homo sapien
45	77	8.7	346	2 Q60044	Q60044 thermotoga

ALIGNMENTS

RESULT 1

ID	Q8PUW8	PRELIMINARY;	PRT;	832 AA.
AC	Q8PUW8;			
DC	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Oligosaccharyl transferase.			
GN	MM2210.			
OS	Methanosarcina mazei (Methanosarcina frisia).			
OC	Archaea; Euryarchaeota; Methanococci; Methanosarcinales;			
OC	Methanosarcinaceae; Methanosarcina.			
OX	NCBI_TaxID=2209;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;			
RX	MEDLINE=22120827; PubMed=12125824;			
RA	Deppeimer U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,			
RA	Martinez-Arias R., Henne A., Wieser A., Baeumer S., Jacobi C.,			
RA	Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,			
RA	Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,			
RA	Fritz H.-J., Gottschalk G.			
RT	"The genome of Methanosarcina mazei: evidence for lateral gene			
RT	transfer between Bacteria and Archaea."			
RL	J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).			
DR	EMBL; AE013461; AAM31906.1; -			
DR	InterPro; IPR003674; Oligo_trans_STT3.			
DR	Pfam; PF02516; STT3; 1			
KW	Transferase; Complete proteome.			
SQ	SEQUENCE 832 AA; 92238 MW; D8B62E2CBFAAFF34 CRC64;			

Query Match	10.3%;	Score 91.5;	DB 17;	Length 832;
Best Local Similarity	27.4%;	Pred. No. 2.8;		
Matches	34;	Conservative	24;	Mismatches 47; Indels 19; Gaps 6;
Qy	22	LCSDSBEEMKALEADFLTNMHTSKISKAHVPSWKVTLNVCVSLVNNLNSPAETGEVHEE	81	
Db	621	LLTDSBEAKTI-----VEKLKVYVMTDTLMAEGKFSITSLSL--AGKEIGEYVEV	669	


```

QY 82 ELVARRKLPALDGFSL--EAML--TIYOLHKICHSAFQHWELIQEDILDTGNDKNGKE 137
DB 670 ETV---KGDGTGRTVATPKQALLQVYKHLK-DGTSLGHPRLVHESAVNSTDDGNSKE 725
QY 138 EVIK 141
DB 726 NTVK 729

RESULT 2
O22880
ID O22880 PRELIMINARY; PRT; 550 AA.
AC O22880;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT2940550 protein.
GN AT2940550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002336; AAB87582.1; -.
SQ SEQUENCE 550 AA; 61321 MW; 721153E2D5FB2126 CRC64;

Query Match 10.1%; Score 90; DB 10; Length 550;
Best Local Similarity 22.2%; Pred. No. 2.4;
Matches 24; Conservative 28; Mismatches 44; Indels 12; Gaps 3;

QY 26 SEEEKALEADPLTNMHTSKSKAHV-----PSWKMTLLNVCSLVNNLNSPAETGEVH 79
DB 436 SEGKSNIPADLVLPQSPQNSLEVIPTETAETWRCYLATCKSLSHSI---GQELQGV 492
QY 80 BEELVARRKLPALDGFSL--EAML--TIYOLHKICHSR--AFQHWELIQE 124
DB 493 ENDLVARRQTSRGLSGQSLRLLTWARMSVSYGETTSLSHQWVLE 540

RESULT 3
O51616
ID O51616 PRELIMINARY; PRT; 171 AA.
AC O51616;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BB0673.
GN BB0673.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;

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RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lachigra B., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Matthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL; AE001168; AAC67020.1; -.
DS TIGR; BB0673; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 171 AA; 20537 MW; 8F7815D05D94E8F6 CRC64;

Query Match 9.8%; Score 87.5; DB 16; Length 171;
Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 44; Conservative 32; Mismatches 55; Indels 39; Gaps 9;

QY 5 MKIQLVCMLLAFS-----SWSLCSDSSEEMK-----ALEADPLTNMHTSKSKA 49
DB 1 MKIQIIMLLALLDFPLNARLLDISIEKRADEIKYSSYNLILEKYYTNFTPTSEIEK- 59
QY 50 HVPWKMTLLNVCSLVNN-----LNSPAETGE-VHEEELVARRKLPALDGFSL--EAML 102
DB 60 --NTYKUTEHFVKSIMLNKNTYSLNSNYKANKYLIQSELDIKKFLKYKI--PKRNIN 115
QY 103 TIYOLHKICHSAFQHWELIQEDILDTGNDKNGKE--EVIKRKIPYILK 149
DB 116 GIFKSHSLIYTKGFKYKLELYIE-----NNAEPLKIFNLNITYFLK 156

RESULT 4
O67377
ID O67377 PRELIMINARY; PRT; 499 AA.
AC O67377;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein AQ_1365.
GN AQ_1365.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aufay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000736; AAC07340.1; -.
DR InterPro; IPR000631; UPF0031.
DR InterPro; IPR004443; YJef_Nterm.
DR Pfam; PF01256; UPF0031.1;
DR Pfam; PF03853; YJef_N; 1.
DR TIGRFAMs; TIGR00196; YJef_Cterm; 1.
DR TIGRFAMs; TIGR00197; YJef_Nterm; 1.
DR PROSITE; PS1050; UPF0031.2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 499 AA; 54371 MW; EDD6B5230AC50F3 CRC64;

Query Match 9.7%; Score 86.5; DB 16; Length 499;
Best Local Similarity 26.5%; Pred. No. 4.8;
Matches 35; Conservative 14; Mismatches 40; Indels 43; Gaps 5;

QY 52 PSWKMTLLNVCSLVNNLNSP-----AEETGEVHEELVARRKLPALDGFSL--EAML 101

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=> s (neurotensin? precursor) or proneurotensin? or preproneurotensin?
L1 83 (NEUROTENSIN? PRECURSOR) OR PRONEUROTENSIN? OR PREPRONEUROTENSIN
?

=> s 11 (12a) human
L2 11 L1 (12A) HUMAN

=> duplicate remove
ENTER L# LIST OR (END):12
DUPLICATE PREFERENCE IS 'BIOSIS, USPATFULL, PCTFULL'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L2
L3 10 DUPLICATE REMOVE L2 (1 DUPLICATE REMOVED)

=> d 1-10

L3 ANSWER 1 OF 10 USPATFULL on STN
AN 2003:154406 USPATFULL
TI Collections of transgenic animal lines (living library)
IN Serafini, Tito Andrew, San Mateo, CA, UNITED STATES
PI US 2003106074 A1 20030605
AI US 2002-77025 A1 20020214 (10)
RLI Continuation-in-part of Ser. No. US 2001-783487, filed on 14 Feb 2001,
PENDING
DT Utility
FS APPLICATION
LN.CNT 5667
INCL INCLM: 800/008.000
INCLS: 800/014.000
NCL NCLM: 800/008.000
NCLS: 800/014.000
IC [7]
ICM: A01K067-033
ICS: A01K067-027
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 10 USPATFULL on STN
AN 2003:72979 USPATFULL
TI Collections of transgenic animal lines (living library)
IN Serafini, Tito Andrew, San Mateo, CA, UNITED STATES
PI US 2003051266 A1 20030313
AI US 2001-783487 A1 20010214 (9)
DT Utility
FS APPLICATION
LN.CNT 4818
INCL INCLM: 800/018.000
INCLS: 435/007.100
NCL NCLM: 800/018.000
NCLS: 435/007.100
IC [7]
ICM: A01K067-027
ICS: G01N033-53
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 10 PCTFULL COPYRIGHT 2004 Univention on STN
AN 2003038049 PCTFULL ED 20030515 EW 200319
TIEN METHOD FOR ISOLATING CELL-TYPE SPECIFIC MRNAS
TIFR METHODE PERMETTANT D'ISOLER DES ARNM SPECIFIQUES D'UN TYPE DE CELLULE
IN HEINTZ, Nathaniel, 441 Fowler Avenue, Pelham Manor, NY 10803, US [US,
US];
SERAFINI, Tito, A., 1835 Mulberry Drive, San Mateo, CA 94403, US [US,
US];
SHYJAN, Andrew, W., 177 Barford Avenue, San Carlos, CA 94070, US [US,
US]
PA RENOVIS, INC., 270 Littlefield Avenue, South San Francisco, CA 94080, US
[US, US], for all designates States except US;
HEINTZ, Nathaniel, 441 Fowler Avenue, Pelham Manor, NY 10803, US [US,
US], for US only;

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SERAFINI, Tito, A., 1835 Mulberry Drive, San Mateo, CA 94403, US [US,
US], for US only;
SHYJAN, Andrew, W., 177 Barford Avenue, San Carlos, CA 94070, US [US,
US], for US only
AG ANTLER, Adriane, M., Pennie & Edmonds LLP, 1155 Avenue of the Americas,
New York, NY 10036, US
LAF English
LA English
DT Patent
PI WO 2003038049 A2 20030508
DS W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ
DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP
KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ
NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ
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SE SK TR
RW (OAPI): BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG
AI WO 2002-US34645 A 20021029
PRAI US 2001-60/340,689 20011029

L3 ANSWER 4 OF 10 PCTFULL COPYRIGHT 2004 Univentio on STN
AN 2002072017 PCTFULL ED 20020927 EW 200238
TIEN METHOD OF DRUG TARGET VALIDATION
TIFR PROCEDE DE VALIDATION DE CIBLES DE MEDICAMENTS
IN SERAFINI, Tito, Andrew, 2249 Bunker Hill Drive, San Mateo, CA
94402-3832, US [US, US]
PA RENOVIS, INC., 270 Littlefield Avenue, South San Francisco, CA 94080, US
[US, US], for all designates States except US;
SERAFINI, Tito, Andrew, 2249 Bunker Hill Drive, San Mateo, CA
94402-3832, US [US, US], for US only
AG ANTLER, Adriane, M., Pennie & Edmonds LLP, 1155 Avenue of the Americas,
New York, NY 10036, US
LAF English
LA English
DT Patent
PI WO 2002072017 A2 20020919
DS W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ
DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP
KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ
NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ
UA UG US UZ VN YU ZA ZM ZW
RW (ARIPO): GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW
RW (EAPO): AM AZ BY KG KZ MD RU TJ TM
RW (EPO): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
RW (OAPI): BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG
AI WO 2002-US7294 A 20020312
PRAI US 2001-60/275,073 20010312

L3 ANSWER 5 OF 10 PCTFULL COPYRIGHT 2004 Univentio on STN
AN 2002064749 PCTFULL ED 20020904 EW 200234
TIEN COLLECTIONS OF TRANSGENIC ANIMAL LINES (LIVING LIBRARY)
TIFR COLLECTIONS DE LIGNEES D'ANIMAUX TRANSGENIQUES (BIBLIOTHEQUE VIVANTE)
IN SERAFINI, Tito, Andrew, 2249 Bunker Hill Drive, San Mateo, CA
94402-3832, US [US, US]
PA RENOVIS, INC., 270 Littlefield Avenue, South San Francisco, CA 94080, US
[US, US], for all designates States except US;
SERAFINI, Tito, Andrew, 2249 Bunker Hill Drive, San Mateo, CA
94402-3832, US [US, US], for US only
AG ANTLER, Adriane, M., Pennie & Edmonds LLP, 1155 Avenue of the Americas,
New York, NY 10036, US
LAF English
LA English
DT Patent
PI WO 2002064749 A2 20020822
DS W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ
DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP

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RW (EAPO): AM AZ BY KG KZ MD RU TJ TM

RW (EPO): AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

RW (OAPI): BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG

AI WO 2002-US4765 A 20020214

PRAI US 2001-09/783,487 20010214

L3 ANSWER 6 OF 10 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1

AN 2001:482536 BIOSIS

DN PREV200100482536

TI Human preproneurotensin/neuromedin N.

AU Lal, Preeti [Inventor]; Shah, Purvi [Inventor]; Corley, Neil C. [Inventor,
Reprint author]

CS Mountain view, CA, USA

ASSIGNEE: Incyte Genomics, Inc.

PI US 6274720 August 14, 2001

SO Official Gazette of the United States Patent and Trademark Office Patents,
(Aug. 14, 2001) Vol. 1249, No. 2. e-file.

CODEN: OGUPE7. ISSN: 0098-1133.

DT Patent

LA English

ED Entered STN: 17 Oct 2001

Last Updated on STN: 23 Feb 2002

L3 ANSWER 7 OF 10 PCTFULL COPYRIGHT 2004 Univentio on STN

AN 2001083691 PCTFULL ED 20020826

TIEN SYSTEM FOR IDENTIFYING AND ANALYZING EXPRESSION OF ARE-CONTAINING GENES

TIFR SYSTEME D'IDENTIFICATION ET D'ANALYSE DE L'EXPRESSION DE GENES CONTENANT
DES ELEMENTS RICHES EN ADENYLATE URIDYLATE (ARE)

IN ABU-KHABAR, Khalid, S.;

WILLIAMS, Bryan, R., G.;

FREVEL, Mathias;

SILVERMAN, Robert, H.

PA THE CLEVELAND CLINIC FOUNDATION;

KING FAISAL SPECIALIST HOSPITAL AND RESEARCH CENTRE;

ABU-KHABAR, Khalid, S.;

WILLIAMS, Bryan, R., G.;

FREVEL, Mathias;

SILVERMAN, Robert, H.

DT Patent

PI WO 2001083691 A2 20011108

DS W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE

DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG

KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ

PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN

YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZW AM AZ BY KG KZ

MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL

PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG

AI WO 2001-US11993 A 20010412

PRAI US 2000-60/196,870 20000412

ICM G06F019-00

ICS G01N033-483

L3 ANSWER 8 OF 10 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 2000:246144 BIOSIS

DN PREV200000246144

TI Comparative sequencing of the proneurotensin gene and association studies
in schizophrenia.

AU Austin, J.; Hoogendoorn, B.; Buckland, P.; Speight, G.; Cardno, A.; Bowen,
T.; Williams, N.; Spurlock, G.; Sanders, R.; Jones, L.; Murphy, K.;

McCarthy, G.; McGuffin, P.; Owen, M. J.; O'Donovan, M. C. [Reprint author]

CS Division of Psychological Medicine, University of Wales College of

Medicine, Heath Park, Cardiff, CF4 4XN, UK

SO Molecular Psychiatry, (March, 2000) Vol. 5, No. 2, pp. 208-212. print.

ISSN: 1359-4184.

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DT Article
LA English
OS Genbank-S47339
ED Entered STN: 14 Jun 2000
Last Updated on STN: 5 Jan 2002

L3 ANSWER 9 OF 10 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:339392 BIOSIS
DN PREV200000339392
TI Association analysis of the proneurotensin gene and bipolar disorder.
AU Austin, J.; Hoogendoorn, B.; Buckland, P.; Jones, I.; McCandless, F.;
Williams, N.; Middle, F.; Owen, M. J.; Craddock, N.; O'Donovan, M. C.
[Reprint author]
CS Division of Psychological Medicine, University of Wales College of
Medicine, Heath Park, Cardiff, CF4 4XN, UK
SO Psychiatric Genetics, (March, 2000) Vol. 10, No. 1, pp. 51-54. print.
ISSN: 0955-8829.

DT Article
LA English
OS Genbank-S47339
ED Entered STN: 10 Aug 2000
Last Updated on STN: 7 Jan 2002

L3 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1999:187752 BIOSIS
DN PREV199900187752
TI Genotyping single nucleotide polymorphisms by primer extension and high
performance liquid chromatography.
AU Hoogendoorn, Bastiaan; Owen, Michael J.; Oefner, Peter J.; Williams,
Nigel; Austin, Jehannine; O'Donovan, Michael C. [Reprint author]
CS Division of Psychological Medicine, University of Wales College of
Medicine, Heath Park, Cardiff, CF4 4XN, UK
SO Human Genetics, (Jan., 1999) Vol. 104, No. 1, pp. 89-93. print.
CODEN: HUGEDQ. ISSN: 0340-6717.

DT Article
LA English
ED Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999

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